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JENKINS, WILSON & TAYLOR, P. A. 3100 TOWER BLVD SUITE 1200 DURHAM, NC 27707			SAKELARIS, SALLY A	
			ART UNIT	PAPER NUMBER
			1634	
DATE MAILED: 02/10/2006				

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/998,058	Applicant(s) THREADGILL ET AL.	
	Examiner Sally A. Sakelaris	Art Unit 1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 02 December 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-27, 46-53 and 61-75 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-27 46-53 61-75 is/are rejected.
- 7) ☒ Claim(s) 74 and 75 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

This action is written in response to applicant's correspondence submitted 4/6/2005. Claims 60, 64, and 70-73 have been amended, claims 28-45 and 54-59 have been canceled, and claims 74 and 75 have been added. Claims 1-27, 46-53, and 61-75 are pending. Applicant's amendments and arguments have been thoroughly reviewed, but are not persuasive for the reasons that follow. Any rejections not reiterated in this action have been withdrawn as necessitated by applicant's amendments to the claims. In light of the Pre-appeals conference that took place on 12/21/2005 several new rejections have been made and can be seen below. This action is non-**Final**.

Claim Objections

Claims 74 and 75 are objected to because of the following informalities: Claim 74 recites two sub step (b)s and excludes a step (a). Appropriate correction is required.

Claim Interpretation

It should be noted that some of the art cited in this office action is intending to relay the breadth of the claims as currently written.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

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1. Claims 8 and 9 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

It is vague and indefinite what is meant by the phrase "less than about 500" and "less than about 100". The phrase "less than" typically indicates a maximum point. The phrase "less than" however, is contraverted by the term "about" which implies that values above and below 500 and 100 nucleotides are permitted. Further, the extent of variance permitted by "about" is unclear in this context. Since nucleotides are whole numbers, "about 500 or 100" cannot mean from 511 to 97.6 because nucleotides cannot be split in half. Therefore, it is also unclear if "about 500 and 100" simply includes 508 or if it also includes 1-508 as well. In Amgen, Inc. v. Chugai Pharmaceutical Co., 927 F.2d 1200 (CAFC 1991), the CAFC stated, "The district court held claims 4 and 6 of the patent invalid because their specific activity limitation of "at least about 160,000" was indefinite". After review, the CAFC states "We therefore affirm the district court's determination on this issue." Thus, the CAFC found the phrase "at least about" indefinite where the metes and bounds of the term were not defined in the specification.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

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2. Claims 1-10, 15, 19-27, 46-53, 64-73 and new claim 75 are rejected under 35

U.S.C. 102(b) as being anticipated by Diehl et al, PNAS 1997.

Diehl et al. teach a method for identifying multiple genetic loci for example, *Col2a1*, *Col1a1* and *Col3a1*(page 5235) that modulate the phenotype of facial clefting in mice. Diehl et al have performed a genome-wide search for loci contributing to susceptibility to teratogen-induced facial clefting in the mouse. AXB and BXA recombinant inbred(RI) lines derived from crosses between A/J and C57BL6/J strains were supplied by M. Nesbitt and the mice were then bred by intercrossing recombinant inbred lines and maintained in a colony at the University of Michigan(page 5232) as a renewable population of genetically diverse individuals. The reference teaches this study for identifying a genetic locus in the diploid mouse system wherein the inbred lines of the renewable population of genetically diverse individuals comprise less than about 100 strains, in one instance a BXD set of 26 RI lines is used(page 5234). Experiments were also performed using the AXB and BXA RI strains to evaluate both spontaneous and teratogen-induced clefting resulting in both visual and physiological phenotypes. The reference uses the extensive data on teratogen-induced clefting in the AXB and BXA RI lines collected previously with a genome wide collection of marker typings for these RI lines to study the effects of genetic polymorphisms segregating in the renewable population(page 5232, left column). Diehl et al. teach the resulting molecular phenotype of their mouse mutants with clefting phenotypes to include for example, eight collagen genes including an altered expression of one, *Col3a1*, which is normally expressed in the embryonic palate. The reference also teaches the method for identifying multiple genetic loci further comprising identifying two or more genetic loci that modulate the phenotype of clefting as seen on the reference's page 5235 in their

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explanation that in addition to *Col3a1*, two other genetic factors, *Colla1* and a cyclic nucleotide phosphodiesterase gene are located on the same chromosome and are thought to together, be possibly relevant to the role of cAMP in the etiology of cleft palate abnormalities(page 5235).

Additionally, the reference teaches the implication of the tenascin C gene, an extracellular matrix protein, and several cell-signaling molecules which have been previously implicated in clefting.

Diehl et al. further teach the modulation of the clefting phenotype by a non-genetic factor that is a drug exposure and an interaction between two or more non-genetic factors that are drug

exposures. The reference reports the findings of a genome-wide search for susceptibility genes for teratogen-induced clefting in the AXB and BXA set of recombinant inbred mouse strains, as they compare the results and the interaction between phenytoin(which induces cleft lip) and 6-

aminonicotinamide(which induces cleft palate) and the cleft palate phenotype(abstract and page 5231). The reference also teaches the method of a non-genetic factors ability to modulate the

clefting phenotype wherein the phenotype is modulated by environmental, non-genetic factors such as a fetus' exposure in utero to ethanol, trimethadione, aminopterin and retinoic acid(page

5231). Included then in these findings are the reference's teachings of the identification of an interaction among two or more non-genetic factors(both environmental and drug-like) and a

genetic locus. Furthermore, as stated previously, this same identification was made among

multiple genetic loci discovered in this study in addition to those gene mutations that are well known in the art that the present reference reiterates, such as *Msx1*, several *Hox* genes, retinoic acid receptor alpha locus etc,(page 5231).

Response to Arguments:

Applicant's arguments filed 4/6/2005 have been fully considered but they are not persuasive. Applicant's first argue that the office is "misinterpreting certain terms in the claims"(Pg. 12), specifically, "the patent office has interpreted "renewable" and "genetically diverse" in ways that are not consistent with how these terms are used in the specification". However, given that the standard for the office is "broadest reasonable interpretation" without the aid of any explicit definition of these terms in the specification, the office believes their interpretation is an accurate one(See *in re Morris*). Applicants go on to assert that the exemplary definitions in their specification provide for their intended definition of these terms. However, again it is asserted that limitations in applicant's arguments, specification etc cannot be read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993). Furthermore, without a requirement for a RI strain in the claims, the art will be applied as broadly as the claims are written. The courts have stated that claims must be given their broadest reasonable interpretation consistent with the specification *In re Morris*, 127 F.3d 1048, 1054-55, 44 USPQ2d 1023, 1027-28 (Fed. Cir. 1997); *In re Prater*, 415 F.2d 1393, 1404-05, 162 USPQ 541, 550-551 (CCPA 1969); and *In re Zletz*, 893 F.2d 319, 321-22, 13 USPQ2d 1320, 1322 (Fed. Cir. 1989) (see MPEP 2111). In addition, while it is obvious that applicant is intending to claim a certain invention, given the broadly drawn claims, it is impossible for the office to interpret the claims as applicant wishes. For example, claim 1 is so generically written that a written work of Gregor Mendel and his pea plants would likely be anticipatory.

3. Claims 1-4 are rejected under 35 U.S.C. 102(b) as being anticipated by Bellamy et al, (Human Genetics, 1991).

Bellamy et al. teach a method for identifying a genetic locus that modulates a phenotype, the method comprising:

(a) providing a renewable population of diploid humans that are genetically diverse individuals; and

(b) mapping the genomes of individuals within the renewable population of genetically diverse individuals that display the phenotype, whereby a genetic locus that modulates the phenotype is identified(Entire document especially pg. 345).

Bellamy et al. further teach the above method wherein the renewable human population of genetically diverse individuals comprises a panel of cell lines derived from genetically diverse individuals(Pg. 341).

Response to Arguments:

Applicant's arguments filed 4/6/2005 have been fully considered but they are not persuasive. Applicant's first argue that the reference fails to show certain features of applicant's invention, it is noted that the features upon which applicant relies (i.e., "phenotype" and "mapping genomes" are not explicitly defined in their claims or specification). Even if there was an exemplary definition, the claims are interpreted in light of the specification, limitations from the specification are not read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993). Furthermore, it is noted that the following two definitions were found in the UC biotech website and show the applicability of the Bellamy reference.

Phenotype: visible characteristic or traits of an organism, like a plant or an animal. Bellamy's teaching of varying band sharing in inbred populations is a visible characteristic resulting from the cutting of a specific restriction enzyme and the subsequent running through an agarose gel.

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Genetic Mapping: determination of the relative locations of genetic information on chromosomes. Bellamy's teaching of the placement and size range of band sharing for first degree relatives in the Gaza family for example, meets the limitation of mapping the genome. The fact that the genetic locus modulates the amount of band sharing is a result of inbreeding populations, but the loci responsible for this apparent modulation between strains are the VNTR loci and specifically "four multi-locus probes, 33.6 and 33.15, (CAC)₅ and M13 were used to produce DNA fingerprints of all or part of the Gaza family"(Pg. 343). The claim does not require that for example, a mutation in the genetic locus in some way alters the expression of the encoded protein causing a aberrant phenotype. As a result the various loci probed in this reference serve to teach the way in which genetic loci modulate the phenotype of band sharing. Furthermore, it should be noted that "determination of the relative locations of genetic information on chromosomes" is such a generic and non-limiting phrase that Bellamy is maintained as applicable. Applicant is encouraged to insert limiting claim language that has basis in their specification so that their claims more clearly depict the inventive concept at issue in the present application.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

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4. Claims 11-14, 16-18, and 64-73 are rejected under 35 U.S.C. 103(a) as being unpatentable over Diehl et al. in view of Dindzans et al.(J. of Immunology, 1986) and in further view of Hedrich, Hans J.(“Genetic Monitoring, 1981).

Diehl et al. teach a method for identifying multiple genetic loci for example, *Col2a1*, *Colla1* and *Col3a1*(page 5235) that modulate the phenotype of facial clefting in mice. Diehl et al have performed a genome-wide search for loci contributing to susceptibility to teratogen-induced facial clefting in the mouse. AXB and BXA recombinant inbred(RI) lines derived from crosses between A/J and C57BL6/J strains were supplied by M. Nesbitt and the mice were then bred by intercrossing recombinant inbred lines and maintained in a colony at the University of Michigan(page 5232) as a renewable population of genetically diverse individuals. The reference teaches this study for identifying a genetic locus in the diploid mouse system wherein the inbred lines of the renewable population of genetically diverse individuals comprise less than about 100 strains, in one instance a BXD set of 26 RI lines is used(page 5234). Experiments were also performed using the AXB and BXA RI strains to evaluate both spontaneous and teratogen-induced clefting resulting in both visual and physiological phenotypes. The reference uses the extensive data on teratogen-induced clefting in the AXB and BXA RI lines collected previously with a genome wide collection of marker typings for these RI lines to study the effects of genetic polymorphisms segregating in the renewable population(page 5232, left column). Diehl et al. teach the resulting molecular phenotype of their mouse mutants with clefting phenotypes to include for example, eight collagen genes including an altered expression of one, *Col3a1*, which is normally expressed in the embryonic palate. The reference also teaches the method for identifying multiple genetic loci further comprising identifying two or more

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genetic loci that modulate the phenotype of clefting as seen on the reference's page 5235 in their explanation that in addition to *Col3a1*, two other genetic factors, *Colla1* and a cyclic nucleotide phosphodiesterase gene are located on the same chromosome and are thought to together, be possibly relevant to the role of cAMP in the etiology of cleft palate abnormalities(page 5235).

Additionally, the reference teaches the implication of the tenascin C gene, an extracellular matrix protein, and several cell-signaling molecules which have been previously implicated in clefting.

Diehl et al. further teach the modulation of the clefting phenotype by a non-genetic factor that is a drug exposure and an interaction between two or more non-genetic factors that are drug exposures. The reference reports the findings of a genome-wide search for susceptibility genes for teratogen-induced clefting in the AXB and BXA set of recombinant inbred mouse strains, as they compare the results and the interaction between phenytoin(which induces cleft lip) and 6-aminonicotinamide(which induces cleft palate) and the cleft palate phenotype(abstract and page 5231). The reference also teaches the method of a non-genetic factors ability to modulate the clefting phenotype wherein the phenotype is modulated by environmental, non-genetic factors such as a fetus' exposure in utero to ethanol, trimethadione, aminopterin and retinoic acid(page 5231). Included then in these findings are the reference's teachings of the identification of an interaction among two or more non-genetic factors(both environmental and drug-like) and a genetic locus. Furthermore, as stated previously, this same identification was made among multiple genetic loci discovered in this study in addition to those gene mutations that are well known in the art that the present reference reiterates, such as *Msx1*, several *Hox* genes, retinoic acid receptor alpha locus etc,(page 5231).

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Diehl et al do not teach the derivation of the RI lines from at least 3, 4 or 8 non-recombinant parent lines or that genetically diverse individuals will be a natural by product from the use of multiple parent strains.

However, Dindzans et al. teach that multiple parents are necessary for the breeding of mice in an attempt to map genes and in the elucidation of mechanisms of genetic control. Dindzans et al. teach “the mode of inheritance of susceptibility/resistance to mouse hepatitis strain 3 (MHV)-3 being determined by typing the set of AXB/BXA recombinant inbred (RI) strain derived from **resistant** A/J and **susceptible** C57BL/6J progenitors for susceptibility to infection as determined by the severity of live pathology”. “The strain distribution pattern for susceptibility showed a discontinuous variation: one strain was fully resistant(like A/J), four strains were fully susceptible (like C57BL/6J), and 16 strains showed an intermediate degree of susceptibility”(page 2355). Accordingly, it has been suggested that strain-dependent susceptibility to MHV-3 reflects genetically controlled immune defects rather than differences in the non-genetic, in this case viral factor. It is important to note the need for parental strain diversity that the reference teaches as “ the AXB/BXA RI strains used in these experiments were derived from susceptible (C57BL/6J) and resistant (A/J) progenitors representing extremes in disease” for the sole purpose of creating RI strains exhibiting distinct patterns of MHV-3 induced liver pathology, and a discontinuous strain distribution pattern of S/R was seen(page 2357, discussion). This reference then teaches the importance of having an “unique assortment of parental genes that are homozygous at every locus, as such strains are useful for the mapping of genes and restriction sites and in the elucidation of mechanisms of genetic control”(page 2355). The reference teaches that multiple progenitors were used to establish their population for the

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expected benefit that using multiple progenitors creates an “unique assortment of parental genes” which is “useful for the mapping of genes and restriction sites and in the elucidation of mechanisms of genetic control”.

Dindzans et al. do not teach the derivation of the RI lines from at least 3, 4 or 8 non-recombinant parent lines.

Hedrich teaches the organization of breeding colonies from a founding colony made up of 8-10 breeding pairs. Hedrich teaches in his Chapter on “genetic monitoring” of the mouse in biomedical research, that the organization of breeding colonies should include propagation steps consisting of three groups: “foundation colony (FC), pedigreed expansion colony (PEC), and production colonies(PC)”(Chapter 8, Page 171). Hedrich further teaches that the “foundation colony, which preserves the germline, should be of limited size” and that it may be either be built up as a single line (SL) or in a modified parallel line(MPL) system. With the SL system, Hedrich teaches that “SL colony members are usually more closely related to each other”. In contrast, Hedrich teaches that “in the MPL system e.g. three family lines are kept for four generations, each consisting of not more than 8-10 breeding pairs”(Pg. 171). The reference continues to teach that “one breeding pair of the foundation colony is selected as common ancestor, whose offspring will again give rise to three family lines” and further that, “the degree of kinship is varying from generation to generation within the cycle”. The reference teaches that this method makes “it possible to select among the lines that one which matches the original standards best”.

Therefore, it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have modified the identification of a genetic locus that modulates

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a phenotype method of Diehl et al. so as to have included the diverse population of non-recombinant, parent lines of Dindzans et al. and to have derived their breeding population from at least 3, 4, or 8 non-recombinant parent lines as taught in further view of Hedrich, not only for the expected benefit that more parents would obviously result in a more diverse progeny, but also for the expected benefit of providing an additional means for furthered variation among mouse lines and for the ability taught by Hedrich of making “it possible to select among the lines that one which matches the original standards best”(Page 171). Therefore, combining the teachings of Diehl et al. in view of Dindzans et al. and in further view of Hedrich would have been obvious at the time the invention was made.

Response to Arguments:

Applicant's arguments considering the deficiency of the cited art to meet the limitations of claims 1 and 2 are acknowledged and are addressed in the above sections of this action. It is maintained that, with respect to applicant's arguments concerning this rejection that the “Dindzans reference does not disclose the production of RI lines from multiple(at least 3, 4, and 8) non-recombinant lines”, and that Hedrich does not remedy this defect in Dindzans. Applicant is reminded that Dindzans was relied upon for its teachings of non-recombinant parental lines in its teaching of “ the AXB/BXA RI strains used in these experiments were derived from susceptible (C57BL/6J) and resistant (A/J) progenitors representing extremes in disease” for the sole purpose of creating RI strains exhibiting distinct patterns of MHV-3 induced liver pathology. The reference thus teaches that multiple progenitors were used to establish their population for the expected benefit that using multiple progenitors creates an “unique assortment of parental genes” which is “useful for the mapping of genes and restriction sites and in the

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elucidation of mechanisms of genetic control". While Hedrich's teaching of 8-10 breeding pairs makes obvious the use of at least 3, 4, or 8 non-recombinant parent lines of Dindzans, not only for the expected benefit that more parents would obviously result in a more diverse progeny, but also for the expected benefit of providing an additional means for furthered variation among mouse lines and for the ability taught by Hedrich of making "it possible to select among the lines that one which matches the original standards best"(Page 171). In response to applicant's argument the office again notes that they are not interpreting the claims as applicant would like considering the standard of the office to give the claims a broadest reasonable interpretation. It should be noted that if applicant were to amend their claims to include the many limitations of their arguments, the art would have less applicability. As they are currently written however, there are not limitations read into them from the specification, arguments, etc. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

5. Claims 1-10, 15, 19-27, 46-53, 60-73 and new claims 74 and 75 are rejected under 35 U.S.C. 103(a) as being unpatentable over Lipp et al.(Journal of APOA International Vol. 82, No.4, 1999) in view of Mettler et al.(US Patent 6,573,438 B1).

With regard to claim 1, Lipp et al teach a method for identifying a genetic locus that modulates a phenotype, the method comprising:

(a) providing a renewable population of genetically diverse individuals(each different soy bean or maize plant), wherein a plurality of the genetically diverse individuals are heterozygous for detectable polymorphism;

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- (b) mapping the genomes(PCR detection of 2 genetic elements) of individuals within the renewable population of genetically diverse individuals that display the phenotype; and
- (c) identifying a genetic locus(35S promoter and the NOS terminator) that modulates the phenotype(insect resistant GMOs) through the mapping step (b).

With regard to claim 3, Lipp et al. teach the above method wherein an individual of the renewable population of genetically diverse individual plants each comprise a diploid organism.

With regard to claim 4, Lipp et al. teach the above method wherein the organism is a plant.

With regard to claim 19, Lipp et al. teach mapping analysis of genetic polymorphisms segregating in the renewable population of genetically diverse individuals such as the many different soy bean and maize plants.

With regard to claims 20 and 21, Lipp et al. teach Roundup Ready[®] Soybeans that contain in-plant tolerance to Roundup[®] brand herbicides, enabling growers to spray labeled brands for Roundup[®] over the top, from emergence throughout flowering, for superior weed control, excellent crop safety and maximum yield potential. Which is to say that those seeds aren't killed by glyphosate, allowing farmers to spray the weed-killer after planting. In addition, the phenotype of the BT-176 Maize includes insecticidal resistance.

With regard to claims 22-27 and 48-53, Lipp et al. teach the phenotypes above and therein also teach the modulation of said phenotypes by non-genetic factors such as considering the maize plants, the environmental influences of poor weather which affects planting and herbicide use, the amount and type of Lepidoptera larvae that is present, and presence of non-target insect and animals that could all modulate the phenotype of the BT-176 Maize plant.

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Furthermore, the two or more genetic loci that were identified to modulate the phenotype include the 35S promoter and the NOS terminator that are both important for the expression of genes and are present in nearly all genetically modified plants(Lipp et al. pg 923).

With regard to claim 46, Lipp et al. teach a method for identifying an interaction between a genetic locus(35S promoter and NOS terminator) and a non-genetic factor such as presence of insects, wherein the interaction modulates a phenotype(ability to act as an insecticide) comprising:

a) providing a renewable population of genetically diverse individuals, wherein a plurality of the genetically divers individuals are heterozygous for a detectable polymorphism(the many soybean and maize plants).

b) providing a non-genetic factor to the renewable population(e.g. poor weather)

c) mapping the genomes of individuals that display the phenotype, whereby an interaction between a genetic locus and the non-genetic factor(also can be considered to be contaminating *A. turmeفاعians* introduced through soil residues on roots see bottom right pg. 924) that modulates a phenotype is identified; and

d) identifying a genetic locus that modulates the phenotype through the mapping and detection of the 35S promoter or NOS terminator.

With regard to claim 60, Lipp et al. teach a method for identifying a genetic locus through PCR amplification of the 35S promoter and the NOS terminator that modulates a phenotype of glyphosate tolerance or insecticide resistance, the method comprising:

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a) providing a renewable population of genetically diverse individuals(soy bean and maize plants), wherein the renewable population of plants comprises plants produced by crossing or backcrossing recombinant inbred lines;

b) mapping the genomes(PCR amplifying these 2 genetic elements characteristic of the genome's GMO status) of plants within a reproducible population of diverse plants that display glyphosate tolerance or insecticide resistance; and

c) identifying a genetic locus that modulates the phenotype through the PCR detection step of b).

With regard to new claims 74 and 75, Lipp et al. teach a method for identifying an interaction between a genetic locus and a non-genetic factor, wherein the interaction modulates a phenotype, the method comprising:

a) providing a renewable population(capable of being bred) of genetically diverse(different) produced by crossing or backcrossing different recombinant inbred lines(as every plant is) wherein the renewable population of genetically diverse individuals are heterozygous for a detectable polymorphism(See table 3 for example, overall method not 100% specific and sensitive, heterozygosity present).

b) providing a non-genetic factor to the renewable population(such as those listed above)

c) mapping the genomes of individuals that display the phenotype, whereby an interaction between a genetic locus and the non-genetic factor(also can be considered to be contaminating *A. turmeffacians* introduced through soil residues on roots see bottom right pg. 924) that modulates a phenotype is identified; and

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d) identifying a genetic locus that modulates the phenotype through the mapping and detection of the 35S promoter or NOS terminator in step c).

Lipp et al.(Journal of APOA International Vol. 82, No.4, 1999) do not teach the method wherein the renewable population of plants are produced by backcrossing recombinant inbred lines comprising less than about 500 lines and further wherein the recombinant inbred lines are derived from at least 3, 4, and 8 different non-recombinant parent lines.

However, Mettler et al.(US Patent 6,573,438 B1) teach these limitations included in claims 2, 8, 9, 11-13, 15-18, 47, and 61-63.

Specifically, with regard to claims 2, 8, 9, 15, and 47 Mettler et al. teach hybrid maize seed produced by crossing plants of an inbred corn line, with plants having a different genotype, and hybrid corn plants produced by growing such hybrid maize seed(Col. 4 lines 44-48).

With regard to claims 11-13, 16-18, 61-63, Mettler et al. also teach that more than 8 recombinant inbred corn lines(e.g. R327H, R372H, R412H, R583H, R660H, 2043 Bt, 2044 Bt, 2070Bt, and 2100Bt) in Col. 4 lines 31-35 can be crossed to provide new hybrid seeds. Therefore, it would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to combine the method of Lipp et al. with the method of Mettler et al. since Mettler et al. teach that their genetically modified Btk expression cassette acting similarly as that discussed in the Lipp et al. reference Bt-176, can be transformed “in any plant and particularly corn, wheat, barley, sorghum, and rice plants and more particularly corn plants derived from a transformant or backcrossing through further breeding experiments”(Col. 9 lines 3-6). As such, the Btk expression cassette would also prove to be similarly detected in the method of Lipp et al. in an attempt to decipher the corn’s GMO status. Furthermore, the Lipp et

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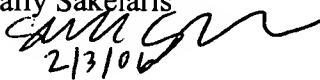
al. reference teaches that their method of identifying 2 genetic elements through PCR(35S promoter and NOS terminator) “seems well suited to serve as a screening method to detect the presence of GMOs” especially since “these 2 genetic elements are important for the expression of genes and are present in nearly all genetically modified plants”(Lipp et al. pg. 923 bottom right).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sally A. Sakelaris whose telephone number is 571-272-0748. The examiner can normally be reached on M-Fri, 9-6:30 1st Friday off.


If attempts to reach the examiner by telephone are unsuccessful, the examiner’s supervisor, Gary Jones can be reached on 571-272-0745. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

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2/3/06



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